

SEQUENCE LISTING

<110> Aventis Pasteur Limited
 Brunham, Robert
 Raudonikiene, Ausra
 Gallichan, Scott
 Murdin, Andrew

<120> Immunization Against Chlamydia Infectio with 60K CRMP

<130> RY185

<150> US 60/481,676

<151> 2003-11-20

<160> 14

<170> PatentIn version 3.3

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<211> 1662

<212> DNA

<213> Chlamydia muridium

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<221> CDS

<222> (1)..(1662)

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Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu	
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gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct	144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala	
35 40 45	
gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca	192
Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala	
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aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act	240
Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr	
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gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt	288
Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe	
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ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc	336
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ggt tgc tgc ttt aca gct gca acg gtt tgt gct tgt cca gag atc cgt Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg 195 200 205			624
tcg gtt acg aaa tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly 210 215 220			672
cca gaa agc gca tgt ttg cgt tgc cca gta act tat aga att aat gta Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val 225 230 235 240			720
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 35 40 45

Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
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Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
 65 70 75 80

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 85 90 95

Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile
 100 105 110

Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile
 115 120 125

Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr
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Gln Gln Leu Pro Cys Glu Ala Gln Phe Val Ser Ser Asp Pro Ala Thr
 145 150 155 160

Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly
 165 170 175

Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu
 180 185 190

Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg

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225	230	235
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Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu		
275	280	285
Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser		
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Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn		
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Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr
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Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly
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Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
20 25 30
gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct 144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
35 40 45

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caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu 115 120 125	384
att act gct aca ggt aaa agg gat tgt gtt gat gtt atc att act cag Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln 130 135 140	432
caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr 145 150 155 160	480
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ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa ggt Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly 180 185 190	576
tgc tgc ttt aca gct gca aca gta tgc gct tgt cca gag atc cgt tcg Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser 195 200 205	624
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gag aat gct tgt ttg cgt tgc cca gta gtt tac aaa att aat ata gtg Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val 225 230 235 240	720
aac caa gga aca gca aca gct cgt aac gtt gtt gtt gaa aat cct gtt Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val 245 250 255	768
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Leu	Gly	Asp	Met	Gln	Pro	Gly	Glu	His	Arg	Thr	Ile	Thr	Val	Glu	Phe		
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tgt	ccg	ctt	aaa	cgt	ggt	cgt	gct	acc	aat	ata	gca	acg	gtt	tct	tac		912
Cys	Pro	Leu	Lys	Arg	Gly	Arg	Ala	Thr	Asn	Ile	Ala	Thr	Val	Ser	Tyr		
	290					295					300						
tgt	gga	gga	cat	aaa	aat	aca	gca	agc	gta	aca	act	gtg	atc	aac	gag		960
Cys	Gly	Gly	His	Lys	Asn	Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn	Glu		
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cct	tgc	gta	caa	gta	agt	att	gca	gga	gca	gat	tgg	tct	tat	gtt	tgt		1008
Pro	Cys	Val	Gln	Val	Ser	Ile	Ala	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys		
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ctt	gaa	gct	gca	gga	gct	caa	att	tct	tgt	aat	aaa	gta	gtt	tgg	act		1152
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Cys	Ser	Asp	Cys	Gly	Thr	Cys	Thr	Ser	Cys	Ala	Glu	Ala	Thr	Thr	Tyr		
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Lys	Glu	Leu	Gln	Pro	Val	Ser	Phe	Ser	Gly	Pro	Thr	Lys	Gly	Thr	Ile		
				485					490					495			
aca	ggc	aat	aca	gta	gta	ttc	gat	tcg	tta	cct	aga	tta	ggt	tct	aaa		1536
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Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val			
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Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg	
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Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
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Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln
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Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
 180 185 190

Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser
 195 200 205

Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro
 210 215 220

Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val
 225 230 235 240

Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val
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Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr
 260 265 270

Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe
 275 280 285

Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr
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Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu
 305 310 315 320

Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys
 325 330 335

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Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn
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Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser
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Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile
 485 490 495

Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys
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Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp
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aaa gag acc act tct cat caa aaa gac aga aaa gca aga aaa aat cat      96
Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His
          20          25          30

caa aat agg act tcc gta gtc cgt aaa gag gtt act gca gtt cgt gat      144
Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp
          35          40          45

act aaa gct gta gag cct aga cag gat tct tgc ttt ggc aaa atg tat      192
Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr
          50          55          60

aca gtc aaa gtt aat gat gat cgt aat gta gaa atc gtg cag tcc gtt      240
Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Val Gln Ser Val
65          70          75          80

cct gaa tat gct acg gta gga tct cca tat cct att gag att act gct      288
Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala
          85          90          95

ata ggg aaa aga gac tgt gtt gat gta atc att aca cag caa tta cca      336
Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro
          100          105          110

tgc gaa gca gag ttt gtt agc agt gat cca gct act act cct act gct      384
Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala
          115          120          125

gat ggt aag cta gtt tgg aaa att gat cgg tta gga cag ggc gaa aag      432
Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys
          130          135          140

agt aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt      480
Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe
145          150          155          160

aca gct gca acg gtt tgt gct tgt cca gag atc cgt tgc gtt acg aaa      528
Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys
          165          170          175

tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt cca gaa agc gca      576
Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala
          180          185          190

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aca gca aca gca cgt aat gtt gtt gtg gaa aat cct gtt cca gat ggc      672
Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly
          210          215          220

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Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu	
245 250 255	
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Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly	
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cac aaa aat act gct agc gta aca aca gtg atc aat gag cct tgc gtg	864
His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val	
275 280 285	
caa gtt aac atc gag gga gca gat tgg tct tat gtt tgt aag cct gta	912
Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val	
290 295 300	
gaa tat gtt atc tct gtt tct aac cct ggt gac tta gtt tta cga gac	960
Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp	
305 310 315 320	
gtt gta att gaa gat acg ctt tct cct gga ata act gtt gtt gaa gca	1008
Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala	
325 330 335	
gct gga gct cag att tct tgt aat aaa ttg gtt tgg act ttg aag gaa	1056
Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu	
340 345 350	
ctc aat cct gga gag tct tta caa tat aag gtt cta gta aga gct caa	1104
Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln	
355 360 365	
act cca ggg caa ttc aca aac aac gtt gtt gtg aaa agt tgc tct gat	1152
Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp	
370 375 380	
tgc ggt att tgt act tct tgc gca gaa gca aca act tac tgg aaa gga	1200
Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly	
385 390 395 400	
gtt gct gct act cat atg tgc gta gta gat act tgt gat cct att tgc	1248
Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys	
405 410 415	
gta gga gag aac act gtt tat cgt atc tgt gtg aca aac aga ggt tct	1296
Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser	
420 425 430	
gct gaa gat aca aat gtg tcc tta att ttg aaa ttc tct aaa gaa tta	1344
Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu	
435 440 445	

caa cct ata tct ttc tct gga cca act aaa gga acc att aca gga aac 1392
 Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn
 450 455 460

acg gta gtg ttt gat tcg tta cct aga tta ggt tct aaa gaa act gta 1440
 Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val
 465 470 475 480

gag ttt tct gta acg ttg aaa gca gta tcc gct gga gat gct cgt ggg 1488
 Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
 485 490 495

gaa gct att ctt tct tcc gat aca ttg aca gtt cct gta tct gat acg 1536
 Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
 500 505 510

gag aat aca cat atc tat 1554
 Glu Asn Thr His Ile Tyr
 515

<210> 6
 <211> 518
 <212> PRT
 <213> Chlamydia muridum

<400> 6

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
 1 5 10 15

Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His
 20 25 30

Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp
 35 40 45

Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr
 50 55 60

Trp Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Val Gln Ser Val
 65 70 75 80

Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala
 85 90 95

Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro
 100 105 110

Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala

115	120	125
Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys 130 135 140		
Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe 145 150 155 160		
Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys 165 170 175		
Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala 180 185 190		
Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly 195 200 205		
Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly 210 215 220		
Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp 225 230 235 240		
Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu 245 250 255		
Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly 260 265 270		
His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val 275 280 285		
Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val 290 295 300		
Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp 305 310 315 320		
Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala 325 330 335		
Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu 340 345 350		

Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln
 355 360 365

Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp
 370 375 380

Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly
 385 390 395 400

Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys
 405 410 415

Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser
 420 425 430

Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu
 435 440 445

Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn
 450 455 460

Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val
 465 470 475 480

Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
 485 490 495

Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
 500 505 510

Glu Asn Thr His Ile Tyr
 515

<210> 7
 <211> 1551
 <212> DNA
 <213> Chlamydia trachomatis

<220>
 <221> CDS
 <222> (1) .. (1551)

<400> 7

atg gag tct ctc tct aca aac gtt att agc tta gct gac acc aaa gcg Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala 1 5 10 15	48
aaa gac aac act tct cat aaa agc aaa aaa gca aga aaa aac cac agc Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser 20 25 30	96
aaa gag act ccc gta gac cgt aaa gag gtt gct ccg gtt cat gag tct Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser 35 40 45	144
aaa gct aca gga cct aaa cag gat tct tgc ttt ggc aga atg tat aca Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr 50 55 60	192
gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca caa gct gtt cct Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro 65 70 75 80	240
gaa tat gct acg gta gga tct ccc tat cct att gaa att act gct aca Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr 85 90 95	288
ggc aaa agg gat tgt gtt gat gtt atc att act cag caa tta cca tgt Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys 100 105 110	336
gaa gca gag ttc gta cgc agt gat cca gcg aca act cct act gct gat Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp 115 120 125	384
ggc aag cta gtt tgg aaa att gac cgc tta gga caa ggc gaa aag agt Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser 130 135 140	432
aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt aca Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr 145 150 155 160	480
gct gca aca gta tgc gct tgt cca gag atc cgt tcg gtt aca aaa tgt Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys 165 170 175	528
gga caa cct gct atc tgt gtt aaa caa gaa ggc cca gag aat gct tgt Gly Gln Pro Ala Ile Cys Val Lys Lys Gln Glu Gly Pro Glu Asn Ala Cys 180 185 190	576
ttg cgt tgc cca gta gtt tac aaa att aat ata gtg aac caa gga aca Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr 195 200 205	624
gca aca gct cgt aac gtt gtt gtt gaa aat cct gtt cca gat ggt tac Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr 210 215 220	672
gct cat tct tct gga cag cgt gta ctg acg ttt act ctt gga gat atg	720

Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met	
225 230 235 240	
caa cct gga gag cac aga aca att act gta gag ttt tgt ccg ctt aaa	768
Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys	
245 250 255	
cgt ggt cgt gct acc aat ata gca acg gtt tct tac tgt gga gga cat	816
Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His	
260 265 270	
aaa aat aca gca agc gta aca act gtg atc aac gag cct tgc gta caa	864
Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln	
275 280 285	
gta agt att gca gga gca gat tgg tct tat gtt tgt aag cct gta gaa	912
Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu	
290 295 300	
tat gtg atc tcc gtt tcc aat cct gga gat ctt gtg ttg cga gat gtc	960
Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val	
305 310 315 320	
gtc gtt gaa gac act ctt tct ccc gga gtc aca gtt ctt gaa gct gca	1008
Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala	
325 330 335	
gga gct caa att tct tgt aat aaa gta gtt tgg act gtg aaa gaa ctg	1056
Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu	
340 345 350	
aat cct gga gag tct cta cag tat aaa gtt cta gta aga gca caa act	1104
Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr	
355 360 365	
cct gga caa ttc aca aat aat gtt gtt gtg aag agc tgc tct gac tgt	1152
Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys	
370 375 380	
ggt act tgt act tct tgc gca gaa gcg aca act tac tgg aaa gga gtt	1200
Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val	
385 390 395 400	
gct gct act cat atg tgc gta gta gat act tgt gac cct gtt tgt gta	1248
Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val	
405 410 415	
gga gaa aat act gtt tac cgt att tgt gtc acc aac aga ggt tct gca	1296
Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala	
420 425 430	
gaa gat aca aat gtt tct tta atg ctt aaa ttc tct aaa gaa ctg caa	1344
Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln	
435 440 445	
cct gta tcc ttc tct gga cca act aaa gga acg att aca ggc aat aca	1392
Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr	

450 455 460

gta gta ttc gat tcg tta cct aga tta ggt tct aaa gaa act gta gag 1440
Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu
465 470 475 480

ttt tct gta aca ttg aaa gca gta tca gct gga gat gct cgt ggg gaa 1488
Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu
 485 490 495

gcg att ctt tct tcc gat aca ttg act gtt cca gtt tct gat aca gag 1536
Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu
 500 505 510

aat aca cac atc tat 1551
Asn Thr His Ile Tyr
 515

<210> 8
<211> 517
<212> PRT
<213> Chlamydia trachomatis

<400> 8

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
1 5 10 15

Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser
 20 25 30

Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser
 35 40 45

Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr
50 55 60

Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro
65 70 75 80

Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr
 85 90 95

Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys
100 105 110

Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp
115 120 125

Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser
 130 135 140

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr
 145 150 155 160

Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys
 165 170 175

Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys
 180 185 190

Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr
 195 200 205

Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr
 210 215 220

Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met
 225 230 235 240

Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys
 245 250 255

Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His
 260 265 270

Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln
 275 280 285

Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu
 290 295 300

Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val
 305 310 315 320

Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala
 325 330 335

Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu
 340 345 350

Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr
 355 360 365

Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys
 370 375 380

Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val
 385 390 395 400

Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val
 405 410 415

Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala
 420 425 430

Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln
 435 440 445

Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr
 450 455 460

Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu
 465 470 475 480

Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu
 485 490 495

Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu
 500 505 510

Asn Thr His Ile Tyr
 515

<210> 9

<211> 37

<212> DNA

<213> Chlamydia muridium

<400> 9

ataagaatgc ggccgcatgc gaataggaga tcctatg

37

<210> 10

<211> 37

<212> DNA

<213> Chlamydia muridium

<400> 10
cgacccaagc ttcatagata tgtgtattct ccgtatc 37

<210> 11
<211> 40
<212> DNA
<213> Chlamydia muridium

<400> 11
ataagaatgc ggccgcatgg agtctctctc taccaacgtt 40

<210> 12
<211> 37
<212> DNA
<213> Chlamydia muridium

<400> 12
cgacccaagc ttcatagata tgtgtattct ccgtatc 37

<210> 13
<211> 31
<212> DNA
<213> Chlamydia muridium

<400> 13
gaattcggat ccgatgaaca aactcatcag a 31

<210> 14
<211> 36
<212> DNA
<213> Chlamydia muridium

<400> 14
attaagaatg cggccgcttc attaatagat atgtgt 36